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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=11; hr=13; min=38; sec=8; ms=962;]

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Application No: 10518414 Version No: 2.0

Input Set:

Output Set:

Started: 2008-02-26 18:40:10.548
Finished: 2008-02-26 18:40:12.027
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 479 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

SEQUENCE LISTING

<110> Chr. Hansen A/S
 Maarten van den Brink, Johannes
 Harboe, Marianne K
 Petersen, Steen Guldager
 Rahbek-Nielsen, Henrik

<120> IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE POLYPEPTIDE IN
 A RECOMBINANT HOST ORGANISM

<130> P1031US00

<140> 10518414

<141> 2005-08-30

<150> PA 2002 0092

<151> 2002-06-17

<160> 10

<170> PatentIn version 3.3

<210> 1

<211> 323

<212> PRT

<213> Bos taurus

<400> 1

Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr
 1 5 10 15

Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu
 20 25 30

Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys
 35 40 45

Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser
 50 55 60

Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly
 65 70 75 80

Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile
 85 90 95

Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp
 100 105 110

Val	Phe	Thr	Tyr	Ala	Glu	Phe	Asp	Gly	Ile	Leu	Gly	Met	Ala	Tyr	Pro			
					115					120					125			
Ser	Leu	Ala	Ser	Glu	Tyr	Ser	Ile	Pro	Val	Phe	Asp	Asn	Met	Met	Asn			
																130	135	140
Arg	His	Leu	Val	Ala	Gln	Asp	Leu	Phe	Ser	Val	Tyr	Met	Asp	Arg	Asn			
																145	150	155 160
Gly	Gln	Glu	Ser	Met	Leu	Thr	Leu	Gly	Ala	Ile	Asp	Pro	Ser	Tyr	Tyr			
																	165	170 175
Thr	Gly	Ser	Leu	His	Trp	Val	Pro	Val	Thr	Val	Gln	Gln	Tyr	Trp	Gln			
																	180	185 190
Phe	Thr	Val	Asp	Ser	Val	Thr	Ile	Ser	Gly	Val	Val	Val	Ala	Cys	Glu			
																	195	200 205
Gly	Gly	Cys	Gln	Ala	Ile	Leu	Asp	Thr	Gly	Thr	Ser	Lys	Leu	Val	Gly			
																210	215	220
Pro	Ser	Ser	Asp	Ile	Leu	Asn	Ile	Gln	Gln	Ala	Ile	Gly	Ala	Thr	Gln			
																225	230	235 240
Asn	Gln	Tyr	Gly	Glu	Phe	Asp	Ile	Asp	Cys	Asp	Asn	Leu	Ser	Tyr	Met			
																	245	250 255
Pro	Thr	Val	Val	Phe	Glu	Ile	Asn	Gly	Lys	Met	Tyr	Pro	Leu	Thr	Pro			
																	260	265 270
Ser	Ala	Tyr	Thr	Ser	Gln	Asp	Gln	Gly	Phe	Cys	Thr	Ser	Gly	Phe	Gln			
																	275	280 285
Ser	Glu	Asn	His	Ser	Gln	Lys	Trp	Ile	Leu	Gly	Asp	Val	Phe	Ile	Arg			
																290	295	300
Glu	Tyr	Tyr	Ser	Val	Phe	Asp	Arg	Ala	Asn	Asn	Leu	Val	Gly	Leu	Ala			
																305	310	315 320
Lys	Ala	Ile																

<210> 2
<211> 1142
<212> DNA
<213> artificial

<220>

<223> DNA fragment comprising a DNA fragment of 1138 bp designed to comprise a N-H-T glycosylation site and unique SalI and XhoI sites for cloning purposes (modB-XS).

<400> 2
cggtcgaccg ctacggtgac tgacacctgg cgtgccgaga tcactcgcat ccccctctac 60

aagggcaagt ctctgcgtaa ggctctcaag gagcacggtc tgctcgagga tttcctgcag 120

aagcagcagt acggcatcag ctctaagtac agcggtttcg gcgagggtggc cagcgtgcct 180

ctcactaact acctggacag ccagtacttc ggtaagatct accttggcac tccccctcag 240

gagttcaccg ttctgttcga tactgggttc agcgacttct gggttccctc catctactgt 300

aagagcaacg cttgcaagaa ccaccagcgc ttcgatcctc gcaagtccag caccttccag 360

aaccttggca agcccccttc catccactac ggtactggca gcatgcaggg tatecttggc 420

tacgacaccg ttaccgtgtc caacatcgtc gatattcagc agaccgtggg tctgagcacc 480

caggagcctg gcgatgtctt cacttacgcc gagttcgatg gtatcctcgg catggcttac 540

ccctccctgg cctctgagta ctctatccct gtgttcgaca acatgatgaa ccgccacctc 600

gtcgctcagg atctgttcag cgtgtacatg gaccgtaacg gtcaggagtc catgcttact 660

ctgggcgcca tcgatccctc ttactacacc ggttccctcc actgggttcc tgtgaccgtc 720

cagcagtact ggcagttcac cgtggacagc gtcactatct ccggcgtggg tgtggcttgc 780

gaggggtggc gtcaggccat ccttgatact ggtaccagca agctcgtcgg cccctccagc 840

gacatcctga acatccagca ggctatcggg gccacccaga accagtacgg cgagttcgat 900

atcgactgcg ataacctttc ttacatgcct actgtggttt tcgagatcaa cggtaagatg 960

taccacctta ctcttctgc ttacacttcc caggatcagg gcttctgtac ctctggtttc 1020

cagtctgaga accacagcca gaagtggatc cttggcgatg tcttcatccg cgagtactac 1080

tccgtcttcg accgtgccaa caacctgggtg ggtctcgcta aggccatctg atcctctaga 1140

gt 1142

<210> 3
<211> 408
<212> DNA
<213> artificial

<220>

<223> an approximately 410 bp SalI-SphII I fragment made using
synthetic oligonucleotides (SEQ ID XXX-1)

<400> 3

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cggtcgaccg ctacggtgac tgacacctgg cgtgccgaga tcactcgcat cccctctac      60
aagggcaagt ctctgcgtaa ggtctctcaag gagcacggtc tgctcgagga tttctctcag    120
aagcagcagt acggcatcag ctctaagtac agcggtttcg gcgagggtggc cagcgtgcct    180
ctcactaact acctggacag ccagtacttc ggtaagatct accttggcac tccccctcag    240
gagttcaccg ttctgttcga tactggttcc agcgacttct gggttccctc catctactgt    300
aagagcaacg cttgcaagaa ccaccagcgc ttcgatccctc gcaagtccag caccttccag    360
aaccttggca agcccccttc catccactac ggtactggca gcatgcag                    408
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<210> 4

<211> 233

<212> DNA

<213> artificial

<220>

<223> an approximately 220 bp SphI-BsrGI fragment made using synthetic
oligonucleotides (SEQ ID XXX-2)

<400> 4

```
gcagcatgca ggggtatcctt ggctacgaca ccgttacctg gtccaacatc gtcgatattc      60
agcagaccgt ggggtctgagc acccaggagc ctggcgatgt cttcacttac gccgagttcg    120
atggtatcct cggcattggct taccctctcc tggcctctga gtactctatc cctgtgttcg    180
acaacatgat gaaccgccac ctctgcgtc aggatctggt cagcgtgtac atg                233
```

<210> 5

<211> 200

<212> DNA

<213> Artificial

<220>

<223> an approximately 190 bp BsrGI-KpnI fragment made using synthetic
oligonucleotides (SEQ ID XXX-3)

<400> 5

```
gcgtgtacat ggaccgtaac ggtcaggagt ccatgcttac tctgggcgcc atcgatccct      60
cttactacac cggttccttc cactgggttc ctgtgaccgt ccagcagtac tggcagttca    120
ccgtggacag cgtcactatc tccggcgtgg ttgtggcttg cgagggtggc tgtcaggcca    180
tccttgatac tggtaccagc                    200
```

<210> 6
<211> 334
<212> DNA
<213> artificial

<220>

<223> an approximately 320 bp KpnI-XbaI fragment made using synthetic oligonucleotides (SEQ ID XXX-4)

<400> 6
ctggtaccag caagctcgtc ggccctcca ggcacatcct gaacatccag caggctatcg 60
gtgccacca gaaccagtac ggcgagttcg atactgactg cgataacctt tcttacatgc 120
ctactgtggt ttctgagatc aacggtaaga tgtacccctt tactccttct gcttacactt 180
cccaggatca gggcttctgt acctctggtt tccagtctga gaaccacagc cagaagtgga 240
tccttggcga tgtcttcacg cgcgagtact actccgtctt cgaccgtgcc aacaacctgg 300
tgggtctcgc taaggccatc tgatcctcta gagt 334

<210> 7
<211> 334
<212> DNA
<213> artificial

<220>

<223> a modified KpnI-XbaI fragment designed for construction of the modBM gene (SEQ ID XXX-5).

<400> 7
ctggtaccag caagctcgtc ggccctcca ggcacatcct gaacatccag caggctatcg 60
gtgccacca gaaccagtac ggcgagttcg atactgactg cgataacctt tcttacatgc 120
ctactgtggt ttctgagatc aacggtaaga tgtacccctt tactccttct gcttacactt 180
cccaggatca gggcttctgt acctctggtt tccagtctga gaaccacacc cagaagtgga 240
tccttggcga tgtcttcacg cgcgagtact actccgtctt cgaccgtgcc aacaacctgg 300
tgggtctcgc taaggccatc tgatcctcta gagt 334

<210> 8
<211> 66
<212> DNA
<213> artificial

<220>

<223> synthetic polylinker (SalI-SphI-BsrGI-KpnI-XbaI) (SEQ ID XXX-6)

<400> 8
ggccaggcgc gccttccatg gaagaatgcg gccgctaaac catcgatggc tcgagttggc 60

gcgccca

66

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 9

catgtacacg ctgaacagat cctgagc

27

<210> 10

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 10

cgtcgaccgc tacggtgact gacacctggc gtaccgacaa ctccaccgag atcactcgca 60

tccccctcta caag

74